

FIG. 1

SECRET

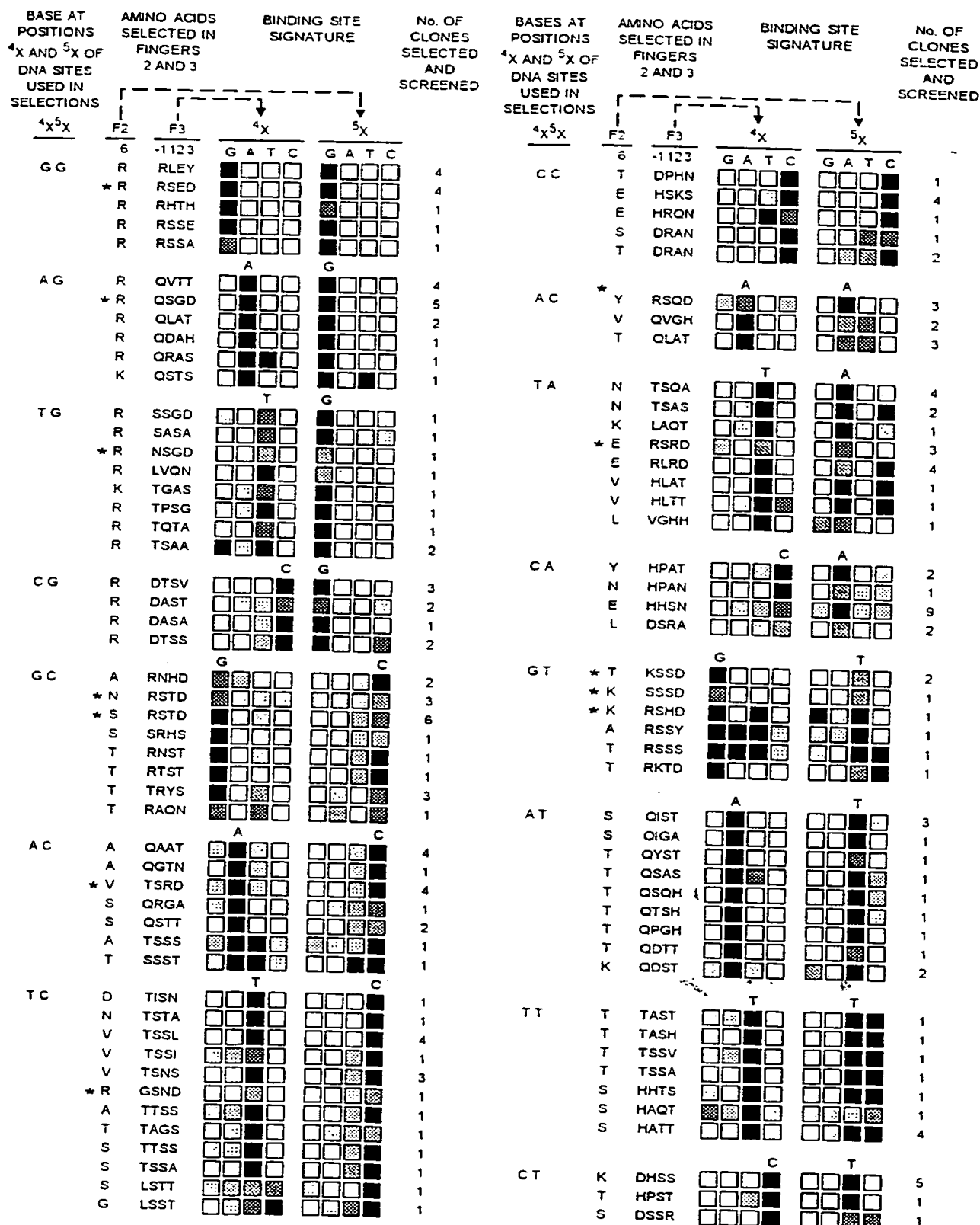
APPROVED	O.G. FIG. 0	
BY	CLASS	SUBCLASS
DRAFTSMAN	435	7.1

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T G Q K P
T G E K P
L R Q K D

FIG. 2

3/6



RELATIVE SIGNATURE STRENGTH ■ ≤1.00 ■ 0.80 ■ 0.60 ■ 0.40 ■ 0.20 ■ 0.00

FIG. 3

4/6

a

AMINO ACID SELECTED AT POSITION -1

BASE PRESENT AT POSITION 4 IN BINDING SIGNATURES	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
G	0	0	0	0	0	0	0	0	1	0	0	0	0	0	16	2	2	0	0	0
A	0	0	0	0	0	0	0	0	0	0	0	0	0	21	1	1	1	0	0	0
T	0	0	0	0	0	1	7	0	0	4	0	1	0	2	5	3	21	1	0	0
C	0	0	10	0	0	0	7	0	0	2	0	0	0	0	2	0	0	0	0	0

↓ C ↓ T/C ↓ T ↓ A G(T) ↓ T

RECOGNITION PATTERNS

b

AMINO ACID SELECTED AT POSITION 6

BASE PRESENT AT POSITION 5 IN BINDING SIGNATURES	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
G	0	0	0	0	0	0	0	0	4	1	0	0	0	0	21	0	0	0	0	0
A	0	0	0	3	0	0	0	0	1	2	0	3	0	0	0	0	2	3	0	2
T	1	0	0	0	0	1	0	0	5	0	0	0	0	0	0	10	17	3	0	0
C	5	0	1	3	0	1	0	0	0	0	0	3	0	0	2	12	14	6	0	0

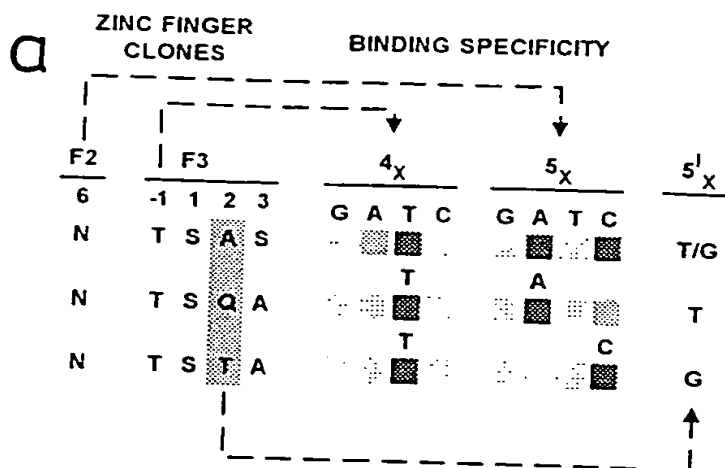
↓ C ↓ A/C ↓ G/T ↓ A/C ↓ G ↓ T/C ↓ C(A/T)

RECOGNITION PATTERNS

FIG. 4

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5/6



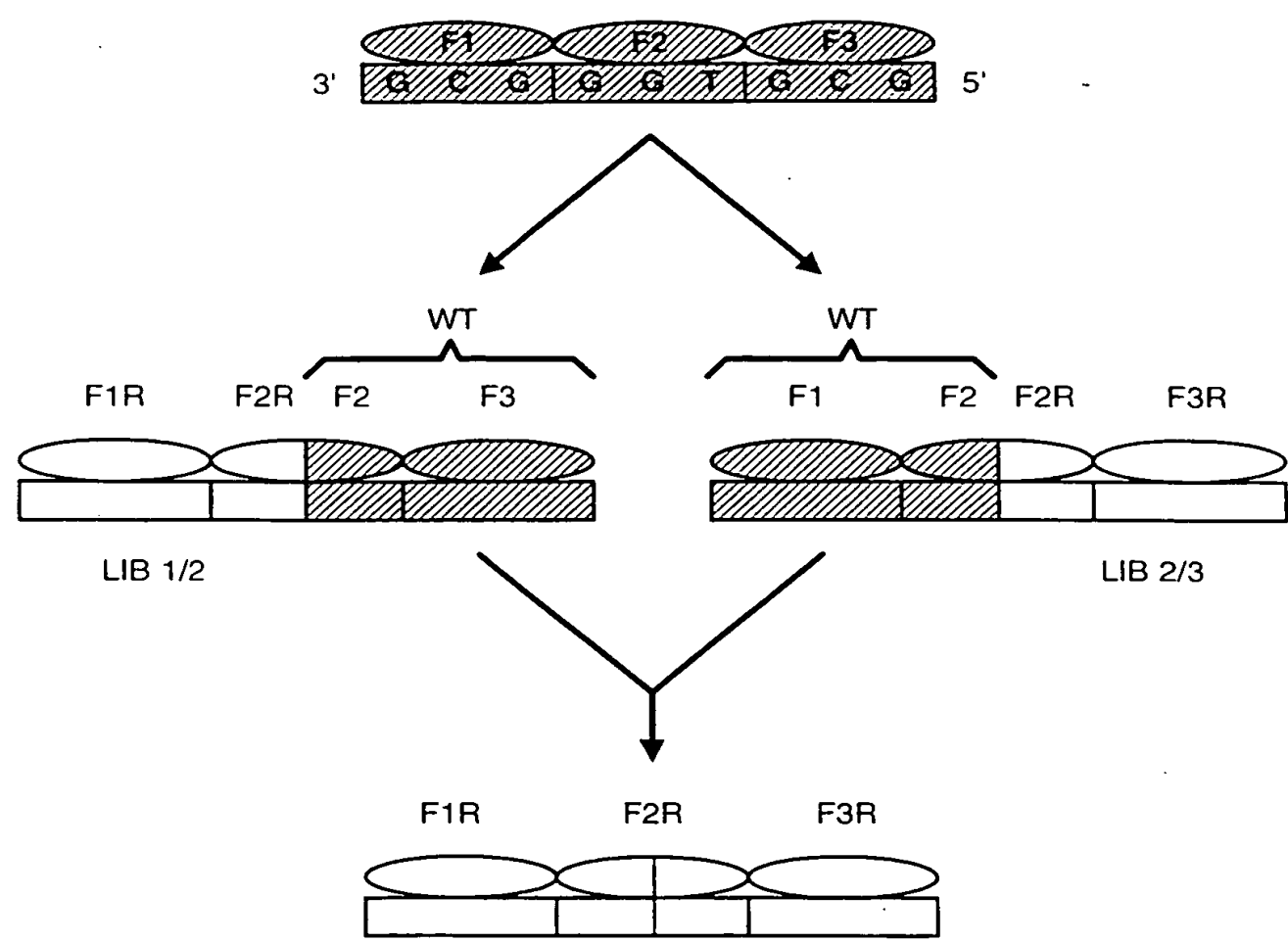
b

AMINO ACID SELECTED AT POSITION 2	F2	F3	CROSS-STRAND BINDING SPECIFICITY	No. OF CLONES SELECTED AND SCREENED
E	6	-1 1 2 3	G A T C	
R	R	R L E Y	■ ■ ■ ■	4
R	R	R S E D	■ ■ ■ ■	4
N	V	T S N S	■ ■ ■ ■	3
N	R	G S N D	■ ■ ■ ■	1
Q	Y	R S Q D	■ ■ ■ ■	3
N	K	T S Q A	■ ■ ■ ■	4
K	L	L A Q T	■ ■ ■ ■	1
T	R	R A Q N	■ ■ ■ ■	1
E	H	R R Q N	■ ■ ■ ■	1
S	H	R A Q T	■ ■ ■ ■	1
R	L	D S R A	■ ■ ■ ■	2
E	R	R S R D	■ ■ ■ ■	3
E	R	R L R D	■ ■ ■ ■	4
V	T	S R R D	■ ■ ■ ■	4
H	A	R N H D	■ ■ ■ ■	2
S	S	R R H S	■ ■ ■ ■	1
T	D	P H H N	■ ■ ■ ■	1
K	E	H S K S	■ ■ ■ ■	4

FIG. 5

006220" 28442460

6 / 6



▨ = wild type Zif268 sequence
R = randomised

FIG.6